K. Haude

1632

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/206,132*

DATE: 10/23/2000
TIME: 23:00:55

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OCT 30 2000

TECH CENTER 1600/2800

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11-21-00
P.2

This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2                                              ENTERED
 3    (1)    General Information:
 4
 5         (i) APPLICANT: Freeman, Gordon J.
 6                        Nadler, Lee M.
 7                        Gray, Gary S.
 8
 9       (ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3
10    WITH INCREASED IMMUNOGENICITY AND USES THEREFOR
11
12      (iii) NUMBER OF SEQUENCES: 8
13
14       (iv) CORRESPONDENCE ADDRESS:
15            (A) ADDRESSEE: LAHIVE & COCKFIELD
16            (B) STREET: 60 State Street, Suite 510
17            (C) CITY: Boston
18            (D) STATE: Massachusetts
19            (E) COUNTRY: USA
20            (F) ZIP: 02109
21
22        (v) COMPUTER READABLE FORM:
23            (A) MEDIUM TYPE: Floppy disk
24            (B) COMPUTER: IBM PC compatible
25            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28       (vi) CURRENT APPLICATION DATA:
29            (A) APPLICATION NUMBER: 09/206,132
30            (B) FILING DATE:
31            (C) CLASSIFICATION:
32
33      (vii) PRIOR APPLICATION DATA:
34            (A) APPLICATION NUMBER: 08/456,104
35            (B) FILING DATE:
36            (A) APPLICATION NUMBER:  08/101,624
37            (B) FILING DATE:   26-JUL-1993
38            (A) APPLICATION NUMBER:  08/109,393
39            (b) FILING DATE:   19-AUG-1993
40
41
42     (viii) ATTORNEY/AGENT INFORMATION:
43            (A) NAME: Mandragouras, Amy E.
44            (B) REGISTRATION NUMBER: 36,207
45            (C) REFERENCE/DOCKET NUMBER: RPI-008
46
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/206,132*

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47          (ix) TELECOMMUNICATION INFORMATION:
48                (A) TELEPHONE: (617) 227-7400
49                (B) TELEFAX: (617) 227-5941
50
51
52
53   (2) INFORMATION FOR SEQ ID NO:1:
54
55        (i) SEQUENCE CHARACTERISTICS:
56                (A) LENGTH: 1120 base pairs
57                (B) TYPE: nucleic acid
58                (C) STRANDEDNESS: single
59                (D) TOPOLOGY: linear
60
61        (ii) MOLECULE TYPE: cDNA
62
63
64        (ix) FEATURE:
65                (A) NAME/KEY: CDS
66                (B) LOCATION: 107..1093
67
68
69        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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71   CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT          60
72
73   GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC           115
74                                                          Met Asp Pro
75                                                           1
76
77   CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG          163
78   Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
79        5                  10                  15
80
81   CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT          211
82   Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
83    20                  25                  30                  35
84
85   GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT          259
86   Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
87                      40                  45                  50
88
89   GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG          307
90   Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
91                  55                  60                  65
92
93   GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG          355
94   Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
95                  70                  75                  80
96
97   GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT          403
98   Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
99        85                  90                  95
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100
101   CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA   451
102   Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
103   100             105             110             115
104
105   AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA   499
106   Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
107               120             125             130
108
109   GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA   547
110   Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile
111           135             140             145
112
113   ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC   595
114   Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr
115           150             155             160
116
117   CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT   643
118   Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr
119       165             170             175
120
121   ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA   691
122   Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu
123   180             185             190             195
124
125   CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG   739
126   Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr
127               200             205             210
128
129   AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT   787
130   Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu
131               215             220             225
132
133   TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA   835
134   Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro
135           230             235             240
136
137   GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT   883
138   Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys
139       245             250             255
140
141   GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG   931
142   Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg
143   260             265             270             275
144
145   CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG   979
146   Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu
147               280             285             290
148
149   AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT   1027
150   Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser
151           295             300             305
152
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/206,132*

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153   GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC        1075
154   Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp
155           310                 315                 320

156
157   AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA                   1120
158   Lys Ser Asp Thr Cys Phe
159       325
160
161
162   (2) INFORMATION FOR SEQ ID NO:2:
163
164           (i) SEQUENCE CHARACTERISTICS:
165                   (A) LENGTH: 329 amino acids
166                   (B) TYPE: amino acid
167                   (D) TOPOLOGY: linear
168
169           (ii) MOLECULE TYPE: protein
170
171           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
172
173   Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
174    1               5                 10                  15
175
176   Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
177               20                  25                  30
178
179   Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
180           35                  40                  45
181
182   Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
183       50                  55                  60
184
185   Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
186    65                  70                  75                  80
187
188   Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
189               85                  90                  95
190
191   Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
192               100                 105                 110
193
194   His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
195           115                 120                 125
196
197   Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
198       130                 135                 140
199
200   Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
201   145                 150                 155                 160
202
203   His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
204               165                 170                 175
205
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INPUT SET: S36032.raw

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206    Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
207                180                 185             190
208
209    Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
210            195                 200                 205
211
212    Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
213        210                 215                 220
214
215    Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
216    225                 230                 235                 240
217
218    Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
219                245                 250                 255
220
221    Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
222                260                 265                 270
223
224    Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
225            275                 280                 285
226
227    Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
228        290                 295                 300
229
230    Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
231    305                 310                 315                 320
232
233    Ser Cys Asp Lys Ser Asp Thr Cys Phe
234                325
235
236    (2) INFORMATION FOR SEQ ID NO:3:
237
238        (i) SEQUENCE CHARACTERISTICS:
239            (A) LENGTH: 1151 base pairs
240            (B) TYPE: nucleic acid
241            (C) STRANDEDNESS: double
242            (D) TOPOLOGY: linear
243
244        (ii) MOLECULE TYPE: cDNA
245
246
247        (ix) FEATURE:
248            (A) NAME/KEY: CDS
249            (B) LOCATION: 99..1028
250
251
252        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
253
254    GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT        60
255
256    CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC                    104
257                                             Met Asp
258                                              1
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/206,132*

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